



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,361  
Source: PG/10  
Date Processed by STIC: 1/4/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

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## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/500,361

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

## RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/10/500,361

TIME: 14:26:29

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

3 <110> APPLICANT: National Institute of Advanced Industrial Science and Technology  
 5 <120> TITLE OF INVENTION: Gene and peptide for transcriptional repressor  
 7 <130> FILE REFERENCE: PH-1684-PCT  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/500,361  
 C--> 9 <141> CURRENT FILING DATE: 2004-06-28  
 9 <150> PRIOR APPLICATION NUMBER: JP 2001-395487  
 10 <151> PRIOR FILING DATE: 2001-12-26  
 12 <150> PRIOR APPLICATION NUMBER: JP 2001-395488  
 13 <151> PRIOR FILING DATE: 2001-12-26  
 15 <150> PRIOR APPLICATION NUMBER: JP 2002-160671  
 W--> 16 <151> PRIOR FILING DATE: (2002-5-31) 2002-05-31 ← use this format for dates  
 18 <160> NUMBER OF SEQ ID NOS: 118

*Suggestion: Consult sequence rules for VALID format*  
**Does Not Comply**  
**Corrected Diskette Needed:**  
 pgs 1-9

## ERRORED SEQUENCES

20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 12  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Nicotiana tabacum  
 W--> 24 <400> SEQUENCE: 1  
 25 Asp Leu Asp Leu Asn Leu Ala Pro Pro Met Glu Phe  
 E--> 26 1      5 5      10      10 ← misaligned numbers - see item 3 on Error Summary sheet  
 42 <210> SEQ ID NO: 4  
 43 <211> LENGTH: 11  
 44 <212> TYPE: PRT  
 45 <213> ORGANISM: artificial  
 W--> 46 <220> FEATURE: → see p. 7 for error explanation (bottom message on p. 7)  
 W--> 46 <223> OTHER INFORMATION:  
 W--> 46 <400> SEQUENCE: 4  
 47 Leu Asp Leu Asn Leu Ala Pro Pro Met Glu Phe  
 E--> 48 1      5 5      10      10 ← misaligned nos.  
 64 <210> SEQ ID NO: 7  
 65 <211> LENGTH: 11  
 66 <212> TYPE: PRT  
 67 <213> ORGANISM: artificial  
 W--> 68 <220> FEATURE: see p. 7  
 W--> 68 <223> OTHER INFORMATION:  
 W--> 68 <400> SEQUENCE: 7  
 69 Leu Asp Leu Asn Leu Ala Ala Ala Ala Ala  
 E--> 70 1      5 5      10      10 ← misaligned  
 129 <210> SEQ ID NO: 16  
 130 <211> LENGTH: 10

p. 2

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,361

DATE: 01/04/2005

TIME: 14:26:29

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

131 <212> TYPE: PRT  
 132 <213> ORGANISM: Arabidopsis thaliana  
 W--> 133 <400> SEQUENCE: 16  
 134 Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala  
 E--> 135 1      5 5 10      10 ← misaligned  
 151 <210> SEQ ID NO: 19  
 152 <211> LENGTH: 8  
 153 <212> TYPE: PRT  
 154 <213> ORGANISM: Arabidopsis thaliana  
 W--> 155 <400> SEQUENCE: 19  
 156 Leu Asp Leu Glu Leu Gly Phe Ala ← misaligned  
 E--> 157 1      5 5  
 159 <210> SEQ ID NO: 20  
 160 <211> LENGTH: (39) 29 shown below  
 161 <212> TYPE: DNA  
 162 <213> ORGANISM: Arabidopsis thaliana  
 W--> 163 <400> SEQUENCE: 20  
 E--> 164 cctggatcta gaactcgggtt tcgcttaag      (39) 29  
 166 <210> SEQ ID NO: 21  
 167 <211> LENGTH: (43) 33  
 168 <212> TYPE: DNA  
 169 <213> ORGANISM: Arabidopsis thaliana  
 W--> 170 <400> SEQUENCE: 21  
 E--> 171 tcgacttaag cgaaaccgag ttctagatcc agg      (43) 33  
 173 <210> SEQ ID NO: 22  
 174 <211> LENGTH: 11  
 175 <212> TYPE: PRT  
 176 <213> ORGANISM: Arabidopsis thaliana  
 W--> 177 <400> SEQUENCE: 22  
 178 Leu Glu Leu Asp Leu Ala Ala Ala Ala Ala  
 E--> 179 1      5 5 10      10 ← misaligned  
 355 <210> SEQ ID NO: 40  
 356 <211> LENGTH: (44) 45 shown  
 357 <212> TYPE: DNA  
 C--> 358 <213> ORGANISM: Artificial Artificial → see p. 7  
 W--> 359 <220> FEATURE:  
 W--> 359 <223> OTHER INFORMATION:  
 W--> 359 <400> SEQUENCE: 40  
 E--> 360 tcggccggct agtcggcggc tagtcggcgg ctagtcggcg (ggatc) (44) 45  
 406 <210> SEQ ID NO: 47  
 407 <211> LENGTH: 24  
 408 <212> TYPE: DNA  
 409 <213> ORGANISM: Arabidopsis thaliana  
 W--> 410 <400> SEQUENCE: 47  
 411 agtgggtcct actgtgtcgg actc 24  
 412 <211> LENGTH: 48  
 E--> 414 <212> TYPE: (39) DNA <211> 39  
 415 <213> ORGANISM: DNA  
 incorrect. Insert correct <213> response

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

OK 416 <400> SEQUENCE: 48  
 417 ccaaataaca ttatcgggtcg actcaaaatt ccataggtg 39  
 E--> 419 <210> SEQ ID NO: 49  
 420 <211> LENGTH: 35  
 421 <212> TYPE: PRT  
 422 <213> ORGANISM: Nicotiana tabacum  
 W--> 423 <400> SEQUENCE: 49  
 424 Val Gly Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gly  
 E--> 425 1 5 10 15 misaligned nos.  
 E--> 426 Tyr Asp Gly Lyn Arg Asp Ile Ala Leu Ala Leu Asn Leu Ala Pro Pro  
 E--> 427 20 25 30  
 428 Met Glu Phe  
 429 35 misaligned  
 447 <210> SEQ ID NO: 52  
 448 <211> LENGTH: 1887  
 449 <212> TYPE: DNA  
 450 <213> ORGANISM: Arabidopdis thaliana  
 W--> 451 <220> FEATURE:  
 452 <221> NAME/KEY: CDS  
 453 <222> LOCATION: (1)(1887)  
 454 <223> OTHER INFORMATION:  
 W--> 455 <300> PUBLICATION INFORMATION:  
 456 <301> AUTHORS: move up to <301> line  
 457 Chao, Q., Rothenberg, M., Solano, R., Roman, G., Terzaghi, W. and Ecker, J.R.  
 458 <302> TITLE: move up to <302> line  
 459 Activation of the ethylene gas response pathway in Arabidopsis by the nuclear  
 protein  
 460 ETHYLENE-INSENSITIVE3 and related proteins  
 461 <303> JOURNAL: Cell  
 462 <304> VOLUME: 89  
 463 <305> ISSUE: (7)  
 464 <306> PAGES: 1133-1144  
 W--> 465 <307> DATE: (1997) invalid date format, per sequence rules  
 466 <308> DATABASE ACCESSION NO: AF004216  
 W--> 467 <300> PUBLICATION INFORMATION: 52  
 468 atg atg ttt aat gag atg gga atg tgt gga aac atg gat ttc ttc tct 48  
 469 Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser  
 W--> 470 1 5 5 10 15 10 15 misaligned  
 471 tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag 96 nos.  
 472 Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu  
 W--> 473 20 25 30  
 474 cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt 144  
 475 Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val  
 W--> 476 35 40 45  
 477 gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt 192  
 478 Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg  
 W--> 479 50 55 60  
 480 ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag 240  
 481 Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln  
 W--> 482 65 70 75 80

\* <3097 error also occurs  
 in sequences 53, 54, 66,  
 69

## RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/500,361

TIME: 14:26:29

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

```

483 agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa 288
484 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
W--> 485      85      90      95
486 gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct 336
487 Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
W--> 488      100     105     110
489 caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act 384
490 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
W--> 491      115     120     125
492 ggt gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt 432
493 Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
W--> 494      130     135     140
495 gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat 480
496 Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
W--> 497 145      150      155      160
498 atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat 528
499 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
W--> 500      165     170     175
501 acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg 576
502 Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
W--> 503      180     185     190
504 ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa 624
505 Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
W--> 506      195     200     205
507 gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct 672
508 Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
W--> 509      210     215     220
510 caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct 720
511 Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
W--> 512 225      230      235      240
513 cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc 768
514 His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
W--> 515      245     250     255
516 aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa 816
517 Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
W--> 518      260     265     270
519 tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg 864
520 Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
W--> 521      275     280     285
522 ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc 912
523 Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
W--> 524      290     295     300
525 gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg 960
526 Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
W--> 527 305      310      315      320
528 atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct 1008
529 Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
W--> 530      325     330     335
531 cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca 1056

```

*Misaligned  
amino acid  
nos.*

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

```

532 His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
W--> 533      340      345      350
534 aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa 1104
535 Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
W--> 536      355      360      365
537 gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga 1152
538 Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
W--> 539      370      375      380
540 gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt 1200
541 Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
W--> 542 385      390      395      400
543 ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg 1248
544 Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
W--> 545      405      410      415
546 aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg 1296
547 Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
W--> 548      420      425      430
549 tat gga gca gca cca tcc agg ttt cat gtc aat gaa gtt aag cct gta 1344
550 Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
W--> 551      435      440      445
552 gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att 1392
553 Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
W--> 554      450      455      460
555 gac tta acg ggt ata gtt cct gaa gat gga cag aag atg atc tca gag 1440
556 Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
W--> 557 465      470      475      480
558 ctc atg tcc atg tac gac aga aat gtc cag agc aac caa acc tct atg 1488
559 Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
W--> 560      485      490      495
561 gtc atg gaa aat caa agc gtg tca ctg ctt caa ccc aca gtc cat aac 1536
562 Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
W--> 563      500      505      510
564 cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc 1584
565 His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
W--> 566      515      520      525
567 ttt gaa gac ttg aac atc cca aac aga gca aac aac aac aac agc agc 1632
568 Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
W--> 569      530      535      540
E--> 570 aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt 1696 1680
571 Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe
W--> 572 545      550      555      560
573 aag ttc gac act gca gat cac aac aac ttt gaa gct gca cat aac aac 1728
574 Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
W--> 575      565      570      575
576 aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca 1776
577 Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
W--> 578      580      585      590
579 ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca 1824
580 Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro

```

*misaligned  
amino  
acid  
nos.*

*IMPORTANT*

## RAW SEQUENCE LISTING

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DATE: 01/04/2005

TIME: 14:26:29

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

W--> 581      595                  600                  605  
 582 gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta 1872  
 583 Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val  
 W--> 584      610                  615                  620  
 585 tcc ata tgg ttc taa                                  1887  
 586 Ser Ile Trp Phe  
 587 625  
 777 <210> SEQ ID NO: 61  
 778 <211> LENGTH: 30  
 779 <212> TYPE: PRT  
 780 <213> ORGANISM: Arabidopsis thaliana  
 OK--> 781 <400> SEQUENCE: 61  
 782 Asn Asp Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu  
 E--> 783      1                          5                          10 10                          15                          15  
 784 Ser Glu Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala  
 E--> 785                          20                          25                          25                          30                          30  
 1311 <210> SEQ ID NO: 118  
 1312 <211> LENGTH: 33  
 1313 <212> TYPE: DNA  
 1314 <213> ORGANISM: artificial  
 W--> 1315 <220> FEATURE:  
 W--> 1315 <223> OTHER INFORMATION:  
 W--> 1315 <400> SEQUENCE: 118  
 1316 tcgactcatt acaaacggag atctagatcc agt      33  
 E--> 1321      40/44

*misaligned nos.**misaligned nos.**see p. 7 for error explanation**delete**FYI: all nucleotides need to be in lower-case letters**all amino acids begin with an upper-case letter, but the remaining letters are in lower-case e.g. Met*



RAW SEQUENCE LISTING ERROR SUMMARY  
 PATENT APPLICATION: US/10/500,361

DATE: 01/04/2005  
 TIME: 14:26:30

*FYI*

Input Set : A:\PTO.YF.txt  
 Output Set: N:\CRF4\01042005\J500361.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:52; Line(s) 459

Seq#:53; Line(s) 600

Seq#:54; Line(s) 666

Skipped Sequences (NEW RULES):

Sequence(s) missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

Seq#:48

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9,39,41,42,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96

Seq#:97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115

Seq#:116,117,118

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:4,5,6,7,8,9,39,40,41,42,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95

Seq#:96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114

Seq#:115,116,117,118

*see p. 8 for more errors  
 and 9 for more errors*

<210> 31  
 <211> 615  
 <212> DNA  
 <213> Arabidopsis thaliana  
 <220>  
 <221> CDS  
 <222> (1) (615)  
 <223>  
 <300>  
 <301> Sakai, H., Medrano, L.J. and Meyerowitz, E.M.  
 <302> Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries  
 <303> Nature  
 <304> 378  
 <305> 6553  
 <306> 199-203  
 <307> 1995  
 <308> U38946  
 <400> 31

<309> and response are MANDATORY whenever <308> has a response

<309>

atg gag aga tca aac agc ata gag ttg agg aac agc ttc tat ggc cgt 48  
 Met Glu Arg Ser Asn Ser Ile Glu Leu Arg Asn Ser Phe Tyr Gly Arg

1

55

10

15  
10

15 ← sample of misaligned amino acid numbers

(all the amino acid nos. are misaligned) in sequence 31

<210> 53  
 <211> 678  
 <212> DNA, ~~PRT~~  
 <213> Nicotiana tabacum  
 <220>  
 <221> CDS  
 <222> (1) (678)  
 <223>  
 <300>

<301> Ohme-Takagi, M. and Shinshi, H.

<302> *move up to <302> line*

Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element

<303> Plant Cell

<304> 7

<305> (2)

<306> 173-182

<307> 1995

<308> D38124

<400> 53

atg gct gtc aaa aat aag gtt agt aat ggc aat ctg aaa gga gga aat 48

Met Ala Val Lys Asn Lys Val Ser Asn Gly Asn Leu Lys Gly Gly Asn

1

5

5

10

15 10

15

*sample of misaligned nos.*

*in the sequence*

*(The above error also appear in sequences 54, 66, 69)*

*This is a DNA sequence. It is a DNA*

*Coding  
Sequence;*

*therefore  
do NOT  
insert PRT  
in <212>  
response*

*insert*

*<309> and response*

## VERIFICATION SUMMARY

DATE: 01/04/2005

PATENT APPLICATION: US/10/500,361

TIME: 14:26:30

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:24 M:283 W: Missing Blank Line separator, <400> field identifier  
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier  
L:39 M:283 W: Missing Blank Line separator, <400> field identifier  
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>  
ORGANISM:artificial  
L:46 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>  
ORGANISM:artificial  
L:46 M:283 W: Missing Blank Line separator, <400> field identifier  
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:46  
L:48 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
L:54 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>  
ORGANISM:artificial  
L:54 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>  
ORGANISM:artificial  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:54 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:54  
L:61 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>  
ORGANISM:artificial  
L:61 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>  
ORGANISM:artificial  
L:61 M:283 W: Missing Blank Line separator, <400> field identifier  
L:61 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:61  
L:68 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>  
ORGANISM:artificial  
L:68 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>  
ORGANISM:artificial  
L:68 M:283 W: Missing Blank Line separator, <400> field identifier  
L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:68  
L:70 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:76 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>  
ORGANISM:artificial  
L:76 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>  
ORGANISM:artificial  
L:76 M:283 W: Missing Blank Line separator, <400> field identifier  
L:76 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:76  
L:83 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>  
ORGANISM:artificial  
L:83 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>  
ORGANISM:artificial  
L:83 M:283 W: Missing Blank Line separator, <400> field identifier  
L:83 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:83  
L:90 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:104 M:283 W: Missing Blank Line separator, <400> field identifier  
L:111 M:283 W: Missing Blank Line separator, <400> field identifier  
L:119 M:283 W: Missing Blank Line separator, <400> field identifier  
L:126 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:283 W: Missing Blank Line separator, <400> field identifier  
L:135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16

L:141 M:283 W: Missing Blank Line separator, <400> field identifier  
L:148 M:283 W: Missing Blank Line separator, <400> field identifier  
L:155 M:283 W: Missing Blank Line separator, <400> field identifier  
L:157 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19  
L:163 M:283 W: Missing Blank Line separator, <400> field identifier  
L:164 M:254 E: No. of Bases conflict, LENGTH:Input:39 Counted:29 SEQ:20  
L:164 M:252 E: No. of Seq. differs, <211> LENGTH:Input:39 Found:29 SEQ:20

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/500,361

DATE: 01/04/2005

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

L:170 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:171 M:254 E: No. of Bases conflict, LENGTH:Input:43 Counted:33 SEQ:21  
 L:171 M:252 E: No. of Seq. differs, <211> LENGTH:Input:43 Found:33 SEQ:21  
 L:177 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:179 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22  
 L:185 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:192 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:199 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:207 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:215 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:222 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:229 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:236 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:243 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:247 M:283 W: Missing Blank Line separator, <300> field identifier  
 L:256 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:31  
 L:256 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:256 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:246  
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
 L:302 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:309 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:316 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:323 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:331 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:339 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:346 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:352 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:39, <213>  
 ORGANISM:Artificial  
 L:352 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:39, <213>  
 ORGANISM:Artificial  
 L:352 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:352 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:352  
 L:358 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40  
 L:359 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:40, <213>  
 ORGANISM:Artificial Sequence  
 L:359 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:40, <213>  
 ORGANISM:Artificial Sequence  
 L:359 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:359 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:359  
 L:360 M:254 E: No. of Bases conflict, LENGTH:Input:44 Counted:45 SEQ:40  
 L:360 M:252 E: No. of Seq. differs, <211> LENGTH:Input:44 Found:45 SEQ:40

# VERIFICATION SUMMARY

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

L:366 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:41, <213>  
 ORGANISM:Artificial  
 L:366 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:41, <213>  
 ORGANISM:Artificial  
 L:366 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:366 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:366  
 L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:42, <213>  
 ORGANISM:Artificial  
 L:374 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:42, <213>  
 ORGANISM:Artificial  
 L:374 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:374 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:374  
 L:382 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:389 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:396 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:403 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:410 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:414 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:416 M:282 E: Numeric Field Identifier Missing, <210> is required.  
 L:416 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:48  
 L:416 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:419 M:214 E: (33) Seq.# missing, SEQ ID NO:48  
 L:425 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49  
 L:426 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 M:332 Repeated in SeqNo=49  
 L:465 M:285 W: Invalid Journal Date Format:Use YYYY-MM-DD,Mon-YYYY,Season-YYYY,or YYYY, SEQ:52  
 L:467 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:52  
 L:467 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:52,Line#:454  
 L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:536 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:539 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/500,361

DATE: 01/04/2005

TIME: 14:26:30

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01042005\J500361.raw

L:545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:554 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:557 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:563 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:569 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:570 M:254 E: No. of Bases conflict, LENGTH:Input:1696 Counted:1680 SEQ:52  
 L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:578 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
 L:608 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:53  
 L:608 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:53,Line#:596  
 L:660 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54  
 L:673 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:54  
 L:673 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:54,Line#:662  
 L:783 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61  
 M:332 Repeated in SeqNo=61  
 L:813 M:112 C: (48) String data converted to lower case,  
 L:820 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:66  
 L:834 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:66  
 L:834 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:66,Line#:822  
 L:904 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:69  
 L:918 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:69  
 L:918 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:69,Line#:906  
 L:1036 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:80, <213>  
 ORGANISM:artificial  
 L:1036 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:80, <213>  
 ORGANISM:artificial  
 L:1036 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:80,Line#:1036  
 L:1044 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:81, <213>  
 ORGANISM:artificial  
 L:1044 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:81, <213>  
 ORGANISM:artificial  
 L:1044 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:81,Line#:1044  
 L:1051 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:82, <213>  
 ORGANISM:artificial  
 L:1051 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:82, <213>  
 ORGANISM:artificial  
 L:1051 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:82,Line#:1051  
 L:1058 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:83, <213>  
 ORGANISM:artificial  
 L:1058 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:83, <213>  
 ORGANISM:artificial  
 L:1058 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:83,Line#:1058  
 L:1066 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:84, <213>  
 ORGANISM:artificial  
 L:1066 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:84, <213>  
 ORGANISM:artificial  
 L:1321 M:254 E: No. of Bases conflict, LENGTH:Input:44 Counted:34 SEQ:118  
 L:1321 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3



L:1321 M:252 E: No. of Seq. differs, <211> LENGTH:Input:33 Found:34 SEQ:118